Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	999	cellulose binding domain or cbd	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 09:15
L2	6185	crystalline cellulose	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 09:16
L3	35335	binding constant or high affinity or affinity constant	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 09:17
L4	15	2 same 3	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 09:17
L5	11	1 and 4	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 09:32
L6	1098	humicola insolens	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 09:32
L7	34	6 same 1	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 10:05
L8	2	4 and 6	US-PGPUB; USPAT	ADJ	OFF	2004/09/13 10:05

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  * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 11:42:45 ON 13 SEP 2004

=> fil .bec
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.42       0.42

FILES 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS, NTIS,
       ESBIOBASE, BIOTECHNO, WPIDS' ENTERED AT 11:43:50 ON 13 SEP 2004
ALL COPYRIGHTS AND RESTRICTIONS APPLY.  SEE HELP USAGETERMS FOR DETAILS.

11 FILES IN THE FILE LIST

=> s cellulose binding domain# or cbd#
FILE 'MEDLINE'
         42323 CELLULOSE
        681369 BINDING
        185335 DOMAIN#
           375 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
          2123 CBD#
L1        2342 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'SCISEARCH'
         37134 CELLULOSE
        631772 BINDING
        334565 DOMAIN#
           587 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
          2090 CBD#
L2        2470 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'LIFESCI'
          9863 "CELLULOSE"
        218703 "BINDING"
         86551 DOMAIN#
           304 CELLULOSE BINDING DOMAIN#
                 ("CELLULOSE"(W)"BINDING"(W)DOMAIN#)
           413 CBD#
L3         584 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'BIOTECHDS'
         10898 CELLULOSE
         32425 BINDING
         13776 DOMAIN#
           271 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
           166 CBD#
L4         319 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'BIOSIS'
         46058 CELLULOSE
        609977 BINDING
        191102 DOMAIN#
           506 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
          1693 CBD#
L5        1996 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'EMBASE'
         26185 "CELLULOSE"
        596117 "BINDING"
```

```
        171534 DOMAIN#
           373 CELLULOSE BINDING DOMAIN#
                 ("CELLULOSE"(W)"BINDING"(W)DOMAIN#)
          2001 CBD#
L6        2204 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'HCAPLUS'
        318460 CELLULOSE
        832290 BINDING
        291331 DOMAIN#
           693 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
          1599 CBD#
L7        1989 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'NTIS'
          3679 CELLULOSE
          9626 BINDING
         21909 DOMAIN#
             4 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
           331 CBD#
L8         334 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'ESBIOBASE'
          6610 CELLULOSE
        224246 BINDING
        112674 DOMAIN#
           324 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
           744 CBD#
L9         905 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'BIOTECHNO'
          9154 CELLULOSE
        277750 BINDING
        111168 DOMAIN#
           361 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
           373 CBD#
L10        574 CELLULOSE BINDING DOMAIN# OR CBD#

FILE 'WPIDS'
         94521 CELLULOSE
         98243 BINDING
         44078 DOMAIN#
           104 CELLULOSE BINDING DOMAIN#
                 (CELLULOSE(W)BINDING(W)DOMAIN#)
           152 CBD#
L11        214 CELLULOSE BINDING DOMAIN# OR CBD#

TOTAL FOR ALL FILES
L12      13931 CELLULOSE BINDING DOMAIN# OR CBD#

=> s crystalline cellulose
FILE 'MEDLINE'
         32876 CRYSTALLINE
         42323 CELLULOSE
L13        257 CRYSTALLINE CELLULOSE
               (CRYSTALLINE(W)CELLULOSE)

FILE 'SCISEARCH'
         98315 CRYSTALLINE
         37134 CELLULOSE
```

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L14          670 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

FILE 'LIFESCI'
            3563 "CRYSTALLINE"
            9863 "CELLULOSE"
L15          287 CRYSTALLINE CELLULOSE
                 ("CRYSTALLINE"(W)"CELLULOSE")

FILE 'BIOTECHDS'
            1468 CRYSTALLINE
           10898 CELLULOSE
L16          323 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

FILE 'BIOSIS'
           20114 CRYSTALLINE
           46058 CELLULOSE
L17          609 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

FILE 'EMBASE'
           13943 "CRYSTALLINE"
           26185 "CELLULOSE"
L18          290 CRYSTALLINE CELLULOSE
                 ("CRYSTALLINE"(W)"CELLULOSE")

FILE 'HCAPLUS'
           65274 CRYSTALLINE
          318608 CRYST
          337814 CRYSTALLINE
                 (CRYSTALLINE OR CRYST)
          318460 CELLULOSE
L19         2737 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

FILE 'NTIS'
            8443 CRYSTALLINE
            3679 CELLULOSE
L20           34 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

FILE 'ESBIOBASE'
            4809 CRYSTALLINE
            6610 CELLULOSE
L21          204 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

FILE 'BIOTECHNO'
            2758 CRYSTALLINE
            9154 CELLULOSE
L22          244 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

FILE 'WPIDS'
           67199 CRYSTALLINE
            1623 CRYST
           68609 CRYSTALLINE
                 (CRYSTALLINE OR CRYST)
           94521 CELLULOSE
L23          1011 CRYSTALLINE CELLULOSE
                 (CRYSTALLINE(W)CELLULOSE)

TOTAL FOR ALL FILES
```

```
L24       6666 CRYSTALLINE CELLULOSE

=> s (binding or affinity) and l12 and l24
FILE 'MEDLINE'
        681369 BINDING
        185677 AFFINITY
L25          58 (BINDING OR AFFINITY) AND L1 AND L13

FILE 'SCISEARCH'
        631772 BINDING
        154199 AFFINITY
L26         110 (BINDING OR AFFINITY) AND L2 AND L14

FILE 'LIFESCI'
        218703 BINDING
         65830 AFFINITY
L27          42 (BINDING OR AFFINITY) AND L3 AND L15

FILE 'BIOTECHDS'
         32425 BINDING
         13666 AFFINITY
L28          28 (BINDING OR AFFINITY) AND L4 AND L16

FILE 'BIOSIS'
        609977 BINDING
        199201 AFFINITY
L29          62 (BINDING OR AFFINITY) AND L5 AND L17

FILE 'EMBASE'
        596117 BINDING
        188439 AFFINITY
L30          57 (BINDING OR AFFINITY) AND L6 AND L18

FILE 'HCAPLUS'
        832290 BINDING
        265012 AFFINITY
L31          83 (BINDING OR AFFINITY) AND L7 AND L19

FILE 'NTIS'
          9626 BINDING
          2446 AFFINITY
L32           1 (BINDING OR AFFINITY) AND L8 AND L20

FILE 'ESBIOBASE'
        224246 BINDING
         67238 AFFINITY
L33          44 (BINDING OR AFFINITY) AND L9 AND L21

FILE 'BIOTECHNO'
        277750 BINDING
         87816 AFFINITY
L34          50 (BINDING OR AFFINITY) AND L10 AND L22

FILE 'WPIDS'
         98243 BINDING
         27438 AFFINITY
L35           2 (BINDING OR AFFINITY) AND L11 AND L23

TOTAL FOR ALL FILES
L36         537 (BINDING OR AFFINITY) AND L12 AND L24

=> s l36 not 2000-2004/py
FILE 'MEDLINE'
       2485271 2000-2004/PY
```

```
L37          46 L25 NOT 2000-2004/PY

FILE 'SCISEARCH'
       4682350 2000-2004/PY
L38          70 L26 NOT 2000-2004/PY

FILE 'LIFESCI'
        472213 2000-2004/PY
L39          36 L27 NOT 2000-2004/PY

FILE 'BIOTECHDS'
         93690 2000-2004/PY
L40          24 L28 NOT 2000-2004/PY

FILE 'BIOSIS'
       2471512 2000-2004/PY
L41          50 L29 NOT 2000-2004/PY

FILE 'EMBASE'
       2162409 2000-2004/PY
L42          48 L30 NOT 2000-2004/PY

FILE 'HCAPLUS'
       4623703 2000-2004/PY
L43          63 L31 NOT 2000-2004/PY

FILE 'NTIS'
         74694 2000-2004/PY
L44           1 L32 NOT 2000-2004/PY

FILE 'ESBIOBASE'
       1348507 2000-2004/PY
L45          31 L33 NOT 2000-2004/PY

FILE 'BIOTECHNO'
        491187 2000-2004/PY
L46          42 L34 NOT 2000-2004/PY

FILE 'WPIDS'
       4162852 2000-2004/PY
L47           0 L35 NOT 2000-2004/PY

TOTAL FOR ALL FILES
L48        411 L36 NOT 2000-2004/PY

=> dup rem l48
PROCESSING COMPLETED FOR L48
L49          103 DUP REM L48 (308 DUPLICATES REMOVED)

=> d tot

L49  ANSWER 1 OF 103  SCISEARCH  COPYRIGHT (c) 2004 The Thomson Corporation.
     on STN
TI   Dynamic interaction of Trichoderma reesei cellobiohydrolases Ce16A and
     Ce17A and cellulose at equilibrium and during hydrolysis
SO   APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (DEC 1999) Vol. 65, No. 12, pp.
     5229-5233.
     Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW,
     WASHINGTON, DC 20005-4171.
     ISSN: 0099-2240.
AU   Palonen H; Tenkanen M; Linder M (Reprint)
AN   1999:949044  SCISEARCH

L49  ANSWER 2 OF 103      MEDLINE on STN                DUPLICATE 1
```

TI Duplicated Clostridium thermocellum cellobiohydrolase gene encoding cellulosomal subunits S3 and S5.
SO Applied microbiology and biotechnology, (1999 Jun) 51 (6) 852-9. Journal code: 8406612. ISSN: 0175-7598.
AU Zverlov V V; Velikodvorskaya G A; Schwarz W H; Kellermann J; Staudenbauer W L
AN 1999351130 MEDLINE

L49 ANSWER 3 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Enzymes, energy, and the environment: A strategic perspective on the US Department of Energy's Research and Development Activities for Bioethanol
SO BIOTECHNOLOGY PROGRESS, (SEP-OCT 1999) Vol. 15, No. 5, pp. 817-827. Publisher: AMER CHEMICAL SOC, 1155 16TH ST, NW, WASHINGTON, DC 20036. ISSN: 8756-7938.
AU Sheehan J; Himmel M (Reprint)
AN 1999:766004 SCISEARCH

L49 ANSWER 4 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Widely different off rates of two closely related **cellulose-binding domains** from Trichoderma reesei
SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (JUN 1999) Vol. 262, No. 3, pp. 637-643. Publisher: BLACKWELL SCIENCE LTD, P O BOX 88, OSNEY MEAD, OXFORD OX2 0NE, OXON, ENGLAND. ISSN: 0014-2956.
AU Carrard G (Reprint); Linder M
AN 1999:512381 SCISEARCH

L49 ANSWER 5 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI The type II and X **cellulose-binding domains** of Pseudomonas xylanase A potentiate catalytic activity against complex substrates by a common mechanism
SO BIOCHEMICAL JOURNAL, (1 SEP 1999) Vol. 342, Part 2, pp. 473-480. Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON W1N 3AJ, ENGLAND. ISSN: 0264-6021.
AU Gill J; Rixon J E; Bolam D N; McQueenMason S; Simpson P J; Williamson M P; Hazlewood G P; Gilbert H J (Reprint)
AN 1999:716106 SCISEARCH

L49 ANSWER 6 OF 103 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Engineering the catalytic and **binding** properties of the cellobiohydrolases from Trichoderma reesei
SO Special Publication - Royal Society of Chemistry (1999), 246(Recent Advances in Carbohydrate Bioengineering), 302-308 CODEN: SROCDO; ISSN: 0260-6291
AU Teeri, T. T.; Divne, C.; Jones, T. A.; Kleywegt, G.; Koivula, A.; Linder, M.; Stahlberg, J.; Von Ossowski, I.; Wohlfahrt, G.; Zou, J.-Y.
AN 2000:29438 HCAPLUS
DN 132:177277

L49 ANSWER 7 OF 103 MEDLINE on STN DUPLICATE 2
TI A beta-1,4-endoglucanase-encoding gene from Cellulomonas pachnodae.
SO Applied microbiology and biotechnology, (1999 Aug) 52 (2) 232-9. Journal code: 8406612. ISSN: 0175-7598.
AU Cazemier A E; Verdoes J C; Op den Camp H J; Hackstein J H; van Ooyen A J
AN 1999429078 MEDLINE

L49 ANSWER 8 OF 103 MEDLINE on STN DUPLICATE 3
TI Active-site mutations which change the substrate specificity of the Clostridium stercorarium cellulase CelZ implications for synergism.
SO European journal of biochemistry / FEBS, (1999 May) 262 (1) 218-23. Journal code: 0107600. ISSN: 0014-2956.

AU Riedel K; Bronnenmeier K
AN 1999248085 MEDLINE

L49 ANSWER 9 OF 103 MEDLINE on STN DUPLICATE 4
TI Endoglucanase 28 (Cel12A), a new Phanerochaete chrysosporium cellulase.
SO European journal of biochemistry / FEBS, (1999 Jan) 259 (1-2) 88-95.
Journal code: 0107600. ISSN: 0014-2956.
AU Henriksson G; Nutt A; Henriksson H; Pettersson B; Stahlberg J; Johansson G; Pettersson G
AN 1999115427 MEDLINE

L49 ANSWER 10 OF 103 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Cellulase core proteins from trichoderma reesei; **binding** properties and efficiency in cellulose hydrolysis
SO Book of Abstracts, 217th ACS National Meeting, Anaheim, Calif., March 21-25 (1999), CELL-018 Publisher: American Chemical Society, Washington, D. C.
CODEN: 67GHA6
AU Tenkanen, Maija; Suurnakki, Anna; Siika-aho, Matti; Palonen, Hetti; Linder, Markus; Kotiranta, Pia; Tjerneld, Folke; Buchert, Johanna; Viikari, Liisa
AN 1999:91347 HCAPLUS

L49 ANSWER 11 OF 103 MEDLINE on STN DUPLICATE 5
TI Design of a pH-dependent **cellulose-binding domain.**
SO FEBS letters, (1999 Mar 19) 447 (1) 13-6.
Journal code: 0155157. ISSN: 0014-5793.
AU Linder M; Nevanen T; Teeri T T
AN 1999232940 MEDLINE

L49 ANSWER 12 OF 103 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Macromolecular assembly of the clostridium thermocellum cellulosome
SO Book of Abstracts, 217th ACS National Meeting, Anaheim, Calif., March 21-25 (1999), CELL-011 Publisher: American Chemical Society, Washington, D. C.
CODEN: 67GHA6
AU Wu, J. H. D.; Lytle, B. L.; Huynh, J. T.
AN 1999:91340 HCAPLUS

L49 ANSWER 13 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Cellulase core proteins from Trichoderma reesei; **binding** properties and efficiency in cellulose hydrolysis; cellobiohydrolase-I and -II and endoglucanase-I and -II for cellulose and kraft pulp hydrolysis (conference abstract)
SO Abstr.Pap.Am.Chem.Soc.; (1999) 217 Meet. Pt.1, CELL018
CODEN: ACSRAL ISSN: 0065-7727
217th ACS National Meeting, American Chemical Society, Anaheim, CA, USA, 21-25 March, 1999.
AU Tenkanen M; Suurnakki A; Siika-aho M; Palonen H; Linder M; Kotiranta P; Tjerneld F; Buchert J; Viikari L
AN 2000-00872 BIOTECHDS

L49 ANSWER 14 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Improved immobilization of fusion proteins via **cellulose-binding domains**
SO BIOTECHNOLOGY AND BIOENGINEERING, (5 DEC 1998) Vol. 60, No. 5, pp. 642-647.
Publisher: JOHN WILEY & SONS INC, 605 THIRD AVE, NEW YORK, NY 10158-0012.
ISSN: 0006-3592.
AU Linder M (Reprint); Nevanen T; Soderholm L; Bengs O; Teeri T T
AN 1998:821748 SCISEARCH

L49 ANSWER 15 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Possible roles for a non-modular, thermostable and proteinase-resistant cellulase from the mesophilic aerobic soil bacterium Cellvibrio mixtus; gene cloning and characterization
SO Appl.Microbiol.Biotechnol.; (1998) 48, 4, 473-79
CODEN: EJABDD ISSN: 0175-7598
AU Fontes C M G A; Clarke J H; Hazlewood G P; Fernandes T H; Gilbert H J; *Ferreira L M A
AN 1998-00315 BIOTECHDS

L49 ANSWER 16 OF 103 MEDLINE on STN DUPLICATE 6
TI Characterization and **affinity** applications of **cellulose -binding domains.**
SO Journal of chromatography. B, Biomedical sciences and applications, (1998 Sep 11) 715 (1) 283-96.
Journal code: 9714109. ISSN: 1387-2273.
AU Tomme P; Boraston A; McLean B; Kormos J; Creagh A L; Sturch K; Gilkes N R; Haynes C A; Warren R A; Kilburn D G
AN 1999007002 MEDLINE

L49 ANSWER 17 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Characterization and **affinity** applications of **cellulose -binding domains**
SO JOURNAL OF CHROMATOGRAPHY B, (11 SEP 1998) Vol. 715, No. 1, pp. 283-296.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0378-4347.
AU Tomme P; Boraston A; McLean B; Kormos J; Creagh A L; Sturch K; Gilkes N R; Haynes C A; Warren R A J; Kilburn D G (Reprint)
AN 1998:772581 SCISEARCH

L49 ANSWER 18 OF 103 MEDLINE on STN DUPLICATE 7
TI Solution structure of the **cellulose-binding domain** of endoglucanase I from Trichoderma reesei and its interaction with cello-oligosaccharides.
SO European journal of biochemistry / FEBS, (1998 Sep 1) 256 (2) 279-86.
Journal code: 0107600. ISSN: 0014-2956.
AU Mattinen M L; Linder M; Drakenberg T; Annila A
AN 1998430965 MEDLINE

L49 ANSWER 19 OF 103 MEDLINE on STN DUPLICATE 8
TI Subcloning and expression of coding region for cellulase **binding** domain of CBH I from P. janthinellum in E. coli.
SO Wei sheng wu xue bao = Acta microbiologica Sinica, (1998 Aug) 38 (4) 269-75.
Journal code: 21610860R. ISSN: 0001-6209.
AU Wang T; Wang C; Gao P; Zhong L; Zou Y
AN 2003042183 MEDLINE

L49 ANSWER 20 OF 103 MEDLINE on STN DUPLICATE 9
TI Synergistic interaction of the cellulosome integrating protein (CipA) from Clostridium thermocellum with a cellulosomal endoglucanase.
SO FEBS letters, (1998 Jan 30) 422 (2) 221-4.
Journal code: 0155157. ISSN: 0014-5793.
AU Ciruela A; Gilbert H J; Ali B R; Hazlewood G P
AN 1998149655 MEDLINE

L49 ANSWER 21 OF 103 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 10
TI Trichoderma reesei cellobiohydrolases: Why so efficient on **crystalline cellulose**?.
SO Biochemical Society Transactions, (May, 1998) Vol. 26, No. 2, pp. 173-178. print.

Meeting Info.: 664th Meeting on Pre- and Post-Partum Nutrition and Metabolism, Enzymology of Cell-Wall Degradation, the Gut as Modulatory Site in Macronutrient Metabolism, Brain-Lipids and Mental Disorders. Reading, England, UK. Biochemical Society.
CODEN: BCSTB5. ISSN: 0300-5127.
AU Teeri, T. T. [Reprint author]; Koivula, K A.; Linder, M.; Wohlfahrt, G.; Divine, C.; Jones, T. A.
AN 1998:328758 BIOSIS

L49 ANSWER 22 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Adsorption of Clostridium stercorarium xylanase A to insoluble xylan and the importance of the **CBDs** to xylan hydrolysis
SO JOURNAL OF FERMENTATION AND BIOENGINEERING, (FEB 1998) Vol. 85, No. 1, pp. 63-68.
Publisher: SOC FERMENTATION BIOENGINEERING, JAPAN, OSAKA UNIV, FACULTY ENGINEERING, 2-1 YAMADAOKA, SUITA, OSAKA 565, JAPAN.
ISSN: 0922-338X.
AU Sun J L; Sakka K (Reprint); Karita S; Kimura T; Ohmiya K
AN 1998:249030 SCISEARCH

L49 ANSWER 23 OF 103 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Structure-function relationships in Trichoderma cellulolytic enzymes
SO Trichoderma and Gliocladium (1998), Volume 2, 3-23. Editor(s): Harman, Gary E.; Kubicek, Christian P. Publisher: Taylor & Francis, London, UK.
CODEN: 66NZAK
AU Koivula, A.; Linder, M.; Teeri, T. T.
AN 1998:722312 HCAPLUS
DN 130:106713

L49 ANSWER 24 OF 103 MEDLINE on STN DUPLICATE 11
TI Evidence for substrate **binding** of a recombinant thermostable xylanase originating from Rhodothermus marinus.
SO FEMS microbiology letters, (1998 Nov 1) 168 (1) 1-7.
Journal code: 7705721. ISSN: 0378-1097.
AU Karlsson E N; Bartonek-Roxa E; Holst O
AN 1999028900 MEDLINE

L49 ANSWER 25 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Surface diffusion of cellulases and their isolated **binding** domains on cellulose
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (19 SEP 1997) Vol. 272, No. 38, pp. 24016-24023.
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.
ISSN: 0021-9258.
AU Jervis E J; Haynes C A; Kilburn D G (Reprint)
AN 97:719837 SCISEARCH

L49 ANSWER 26 OF 103 MEDLINE on STN DUPLICATE 12
TI CelG from Clostridium cellulolyticum: a multidomain endoglucanase acting efficiently on **crystalline cellulose.**
SO Journal of bacteriology, (1997 Nov) 179 (21) 6595-601.
Journal code: 2985120R. ISSN: 0021-9193.
AU Gal L; Gaudin C; Belaich A; Pages S; Tardif C; Belaich J P
AN 1998012954 MEDLINE

L49 ANSWER 27 OF 103 MEDLINE on STN DUPLICATE 13
TI Analysis of xysA, a gene from Streptomyces halstedii JM8 that encodes a 45-kilodalton modular xylanase, Xys1.
SO Applied and environmental microbiology, (1997 Aug) 63 (8) 2983-8.
Journal code: 7605801. ISSN: 0099-2240.
AU Ruiz-Arribas A; Sanchez P; Calvete J J; Raida M; Fernandez-Abalos J M;

Santamaria R I
AN 97394924 MEDLINE

L49 ANSWER 28 OF 103 MEDLINE on STN DUPLICATE 14
TI Cloning and sequence analysis of genes encoding xylanases and acetyl xylan esterase from Streptomyces thermoviolaceus OPC-520.
SO Applied and environmental microbiology, (1997 Feb) 63 (2) 661-4.
Journal code: 7605801. ISSN: 0099-2240.
AU Tsujibo H; Ohtsuki T; Iio T; Yamazaki I; Miyamoto K; Sugiyama M; Inamori Y
AN 97176398 MEDLINE

L49 ANSWER 29 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Interaction between Clostridium thermocellum endoglucanase CelD and polypeptides derived from the cellulosome-integrating protein CipA: stoichiometry and cellulolytic activity of the complexes
SO BIOCHEMICAL JOURNAL, (1 SEP 1997) Vol. 326, Part 2, pp. 617-624.
Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON, ENGLAND W1N 3AJ.
ISSN: 0264-6021.
AU Kataeva I; Guglielmi G; Beguin P (Reprint)
AN 97:672360 SCISEARCH

L49 ANSWER 30 OF 103 MEDLINE on STN DUPLICATE 15
TI Two genes encoding an endoglucanase and a cellulose-**binding** protein are clustered and co-regulated by a TTA codon in Streptomyces halstedii JM8.
SO Biochemical journal, (1997 Jun 1) 324 (Pt 2) 403-11.
Journal code: 2984726R. ISSN: 0264-6021.
AU Garda A L; Fernandez-Abalos J M; Sanchez P; Ruiz-Arribas A; Santamaria R I
AN 97307849 MEDLINE

L49 ANSWER 31 OF 103 MEDLINE on STN DUPLICATE 16
TI Three-dimensional structures of three engineered **cellulose-binding domains** of cellobiohydrolase I from Trichoderma reesei.
SO Protein science : a publication of the Protein Society, (1997 Feb) 6 (2) 294-303.
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AN 93066164 MEDLINE

L49 ANSWER 87 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN

TI ANALYSIS OF FUNCTIONAL DOMAINS OF ENDOGLUCANASES FROM CLOSTRIDIUM-CELLULOVORANS BY GENE CLONING, NUCLEOTIDE SEQUENCING AND CHIMERIC PROTEIN CONSTRUCTION
SO MOLECULAR & GENERAL GENETICS, (FEB 1992) Vol. 231, No. 3, pp. 472-479. ISSN: 0026-8925.
AU HAMAMOTO T; FOONG F; SHOSEYOV O; DOI R H (Reprint)
AN 92:127423 SCISEARCH

L49 ANSWER 88 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI The molecular architecture of xylanases from Pseudomonas fluorescens subsp. cellulosa;
endo-1,4-beta-D-xylanase, alpha-L-arabinofuranosidase and acetylesterase characterization and gene cloning (conference paper)
SO Prog.Biotechnol.; (1992) 7, 259-73
CODEN: PBITE3
AU Hazlewood G P; Gilbert H J
AN 1994-10112 BIOTECHDS

L49 ANSWER 89 OF 103 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI Identification of the **cellulose-binding domain** of the cellulosome subunit S1 from Clostridium thermocellum YS.
SO FEMS (Federation of European Microbiological Societies) Microbiology Letters, (1992) Vol. 99, No. 2-3, pp. 181-186.
CODEN: FMLED7. ISSN: 0378-1097.
AU Poole, Debbie M.; Morag, Ely; Lamed, Raphael; Bayer, Edward A.; Hazlewood, Geoffrey P.; Gilbert, Harry J. [Reprint author]
AN 1993:122258 BIOSIS

L49 ANSWER 90 OF 103 MEDLINE on STN DUPLICATE 51
TI Biochemistry and genetics of actinomycete cellulases.
SO Critical reviews in biotechnology, (1992) 12 (1-2) 45-63. Ref: 73
Journal code: 8505177. ISSN: 0738-8551.
AU Wilson D B
AN 92127620 MEDLINE

L49 ANSWER 91 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Studies of Thermomonospora fusca cellulases;
CM-cellulase and cellobiohydrolase purification and characterization, and gene cloning and expression in Escherichia coli and Streptomyces lividans (conference abstract)
SO Abstr.Pap.Am.Chem.Soc.; (1992) 203 Meet., Pt.1, BIOT17
CODEN: ACSRAL
AU Lao G; McGinnis K; Spezio M; Wilson D
AN 1992-08771 BIOTECHDS

L49 ANSWER 92 OF 103 MEDLINE on STN DUPLICATE 52
TI The cellodextrinase from Pseudomonas fluorescens subsp. cellulosa consists of multiple functional domains.
SO Biochemical journal, (1991 Nov 1) 279 (Pt 3) 793-9.
Journal code: 2984726R. ISSN: 0264-6021.
AU Ferreira L M; Hazlewood G P; Barker P J; Gilbert H J
AN 92061996 MEDLINE

L49 ANSWER 93 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI ENGINEERING OF ENZYMES OF CARBOHYDRATE-METABOLISM
SO CURRENT OPINION IN BIOTECHNOLOGY, (1991) Vol. 2, No. 4, pp. 614-621.
AU TEERI T T (Reprint)
AN 91:541856 SCISEARCH

L49 ANSWER 94 OF 103 MEDLINE on STN DUPLICATE 53
TI The non-catalytic C-terminal region of endoglucanase E from Clostridium thermocellum contains a **cellulose-binding**

domain.
SO Biochemical journal, (1991 Jan 15) 273(Pt 2) 289-93.
Journal code: 2984726R. ISSN: 0264-6021.
AU Durrant A J; Hall J; Hazlewood G P; Gilbert H J
AN 91119553 MEDLINE

L49 ANSWER 95 OF 103 MEDLINE on STN DUPLICATE 54
TI The 1,4-beta-D-glucan cellobiohydrolases from Phanerochaete chrysosporium. I. A system of synergistically acting enzymes homologous to Trichoderma reesei.
SO Journal of biotechnology, (1991 Jul) 19 (2-3) 271-85.
Journal code: 8411927. ISSN: 0168-1656.
AU Uzcategui E; Ruiz A; Montesino R; Johansson G; Pettersson G
AN 91273927 MEDLINE

L49 ANSWER 96 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI THE 1,4-BETA-D-GLUCAN CELLOBIOHYDROLASES FROM PHANEROCHAETE-CHRYSOSPORIUM .1. A SYSTEM OF SYNERGISTICALLY ACTING ENZYMES HOMOLOGOUS TO TRICHODERMA-REESEI
SO JOURNAL OF BIOTECHNOLOGY, (1991) Vol. 19, No. 2-3, pp. 271-285.
AU UZCATEGUI E; RUIZ A; MONTESINO R; JOHANSSON G; PETTERSSON G (Reprint)
AN 91:358788 SCISEARCH

L49 ANSWER 97 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Purification and characterization of fungal cellulases;
cellulase complex isolation from Fusarium, Humicola and Mycelopthera spp. (conference abstract)
SO Abstr.Pap.Am.Chem.Soc.; (1991) 202 Meet., Pt.1, BIOT187
CODEN: ACSRAL
AU Schuelein M; Schou C; Rasmussen G
AN 1991-14350 BIOTECHDS

L49 ANSWER 98 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI How do Trichoderma reesei cellobiohydrolases bind to and degrade cellulose (query);
cellobiohydrolase and cellulase characterization (conference abstract)
SO Abstr.Pap.Am.Chem.Soc.; (1991) 202 Meet., Pt.1, BIOT206
CODEN: ACSRAL
AU Reinikainen T R; Ruohonen L; Koivula A; Srisodsuk M; Jones A; Knowles J K C
AN 1991-14356 BIOTECHDS

L49 ANSWER 99 OF 103 MEDLINE on STN DUPLICATE 55
TI The N-terminal region of an endoglucanase from Pseudomonas fluorescens subspecies cellulosa constitutes a **cellulose-binding domain** that is distinct from the catalytic centre.
SO Molecular microbiology, (1990 May) 4 (5) 759-67.
Journal code: 8712028. ISSN: 0950-382X.
AU Gilbert H J; Hall J; Hazlewood G P; Ferreira L M
AN 90355836 MEDLINE

L49 ANSWER 100 OF 103 MEDLINE on STN DUPLICATE 56
TI Xylanase B and an arabinofuranosidase from Pseudomonas fluorescens subsp. cellulosa contain identical **cellulose-binding domains** and are encoded by adjacent genes.
SO Biochemical journal, (1990 Dec 1) 272 (2) 369-76.
Journal code: 2984726R. ISSN: 0264-6021.
AU Kellett L E; Poole D M; Ferreira L M; Durrant A J; Hazlewood G P; Gilbert H J
AN 91097447 MEDLINE

L49 ANSWER 101 OF 103 MEDLINE on STN DUPLICATE 57
TI Spatial separation of protein domains is not necessary for catalytic

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     activity or substrate binding in a xylanase.
SO   Biochemical journal, (1990 Jul 1) 269 (1) 261-4.
     Journal code: 2984726R. ISSN: 0264-6021.
AU   Ferreira L M; Durrant A J; Hall J; Hazlewood G P; Gilbert H J
AN   90328982     MEDLINE

L49   ANSWER 102 OF 103  BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI    Structural and functional aspects of cellulases from a cellulolytic
      bacterium;
         Cellulomonas fimi cellulase characterization (conference abstract)
SO    Abstr.Pap.Am.Chem.Soc.; (1989) 198 Meet., MBTD40
      CODEN: ACSRAL
AU    Gilkes N R; Kilburn D G; Miller Jr R C; Warren R A J
AN    1990-00472  BIOTECHDS

L49    ANSWER 103 OF 103 NTIS COPYRIGHT 2004 NTIS on STN
TI     Computer-Aided Protein Modelling: Applications to Antibody and Enzyme
       Engineering. Thesis.
NR     PB95-129706/XAB; VTT/PUB-185, ISBN-951-38-4623-7
       148p; c1994
AU     Hoffren, A. M.
AN     1995(14):05754   NTIS


=> s humicola insolens
FILE 'MEDLINE'
          271 HUMICOLA
           59 INSOLENS
L50        55 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'SCISEARCH'
          632 HUMICOLA
          116 INSOLENS
L51       105 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'LIFESCI'
          341 "HUMICOLA"
           54 "INSOLENS"
L52        42 HUMICOLA INSOLENS
                ("HUMICOLA"(W)"INSOLENS")

FILE 'BIOTECHDS'
          597 HUMICOLA
          114 INSOLENS
L53       113 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'BIOSIS'
         1137 HUMICOLA
          201 INSOLENS
L54       143 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'EMBASE'
          295 "HUMICOLA"
           52 "INSOLENS"
L55        52 HUMICOLA INSOLENS
                ("HUMICOLA"(W)"INSOLENS")

FILE 'HCAPLUS'
         1314 HUMICOLA
          290 INSOLENS
```

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L56         278 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'NTIS'
              4 HUMICOLA
              0 INSOLENS
L57           0 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'ESBIOBASE'
            224 HUMICOLA
             55 INSOLENS
L58          50 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'BIOTECHNO'
            227 HUMICOLA
             44 INSOLENS
L59          42 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

FILE 'WPIDS'
            362 HUMICOLA
             97 INSOLENS
L60          81 HUMICOLA INSOLENS
                (HUMICOLA(W)INSOLENS)

TOTAL FOR ALL FILES
L61         961 HUMICOLA INSOLENS

=> s l12 and l61
FILE 'MEDLINE'
L62           5 L1 AND L50

FILE 'SCISEARCH'
L63          11 L2 AND L51

FILE 'LIFESCI'
L64           6 L3 AND L52

FILE 'BIOTECHDS'
L65          16 L4 AND L53

FILE 'BIOSIS'
L66           9 L5 AND L54

FILE 'EMBASE'
L67           7 L6 AND L55

FILE 'HCAPLUS'
L68          32 L7 AND L56

FILE 'NTIS'
L69           0 L8 AND L57

FILE 'ESBIOBASE'
L70           7 L9 AND L58

FILE 'BIOTECHNO'
L71           7 L10 AND L59

FILE 'WPIDS'
L72          14 L11 AND L60
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TOTAL FOR ALL FILES
L73         114 L12 AND L61

=> s l73 not 2000-2004/py
FILE 'MEDLINE'
       2485271 2000-2004/PY
L74           5 L62 NOT 2000-2004/PY

FILE 'SCISEARCH'
       4682350 2000-2004/PY
L75           6 L63 NOT 2000-2004/PY

FILE 'LIFESCI'
        472213 2000-2004/PY
L76           4 L64 NOT 2000-2004/PY

FILE 'BIOTECHDS'
         93690 2000-2004/PY
L77          12 L65 NOT 2000-2004/PY

FILE 'BIOSIS'
       2471512 2000-2004/PY
L78           5 L66 NOT 2000-2004/PY

FILE 'EMBASE'
       2162409 2000-2004/PY
L79           5 L67 NOT 2000-2004/PY

FILE 'HCAPLUS'
       4623703 2000-2004/PY
L80          11 L68 NOT 2000-2004/PY

FILE 'NTIS'
         74694 2000-2004/PY
L81           0 L69 NOT 2000-2004/PY

FILE 'ESBIOBASE'
       1348507 2000-2004/PY
L82           5 L70 NOT 2000-2004/PY

FILE 'BIOTECHNO'
        491187 2000-2004/PY
L83           5 L71 NOT 2000-2004/PY

FILE 'WPIDS'
       4162852 2000-2004/PY
L84           3 L72 NOT 2000-2004/PY

TOTAL FOR ALL FILES
L85          61 L73 NOT 2000-2004/PY

=> dup rem l85
PROCESSING COMPLETED FOR L85
L86           24 DUP REM L85 (37 DUPLICATES REMOVED)

=> d tot

L86   ANSWER 1 OF 24  BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI    Modified enzyme for laundry detergents and/or fabric care compositions
      for e.g. cleaning, stain removal, whiteness maintenance, fabric softness,
      color appearance and fabric wear properties;
         containing a cellulolytic enzyme and a cellulose-
         binding domain from Cellulomonas sp., Trichoderma
         sp., Clostridium sp., Thermonospora sp., Bacillus sp. and Humicola sp.
```

AU Busch A; Bettiol J L P; Smets J; Boyer S L
AN 2000-03361 BIOTECHDS
PI WO 9957256 11 Nov 1999

L86 ANSWER 2 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Modified enzyme for laundry detergents and/or fabric care compositions for e.g. cleaning, stain removal, whiteness maintenance, fabric softness, color appearance and fabric antiwear properties;
cellulase production and characterization from **Humicola insolens** or Trichoderma reesei with a **cellulose binding domain** for use in laundry surfactant
AU Busch A; Bettiol J L; Smets J; Boyer S L
AN 2000-02690 BIOTECHDS
PI WO 9957260 11 Nov 1999

L86 ANSWER 3 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Modified enzyme for laundry detergent, fabric care composition;
Humicola insolens cellulase and an e.g. Cellulomonas fimi, Clostridium cellulolyticum or Myxoccus xanthus **cellulose-binding domain** for use in a laundry surfactant
AU Smets J; Busch A; Baeck A C; Bettiol J L; Boyer S L
AN 2000-02689 BIOTECHDS
PI WO 9957259 11 Nov 1999

L86 ANSWER 4 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Modified enzyme, useful e.g. in washing, cleaning and/or fabric care methods including anti-wrinkle, anti-bobbling and anti-shrinkage properties, for static control, fabric softness and color appearance;
surfactant comprising **cellulose binding domain** and an enzyme e.g. lipase, protease, amylase, etc.
AU Smets J; Bettiol J L P; Boyer S L; Busch A
AN 2000-02660 BIOTECHDS
PI WO 9957252 11 Nov 1999

L86 ANSWER 5 OF 24 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Environmental friendly laundry detergent compositions comprising a specific cellulase and a nil-phosphate containing chelant
SO PCT Int. Appl., 74 pp.
CODEN: PIXXD2
IN Bettiol, Jean-Luc Philippe; Thoen, Christiaan Arthur Jacques Kamiel; Convents, Andre Christian
AN 1999:64891 HCAPLUS
DN 130:126610

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9902636	A1	19990121	WO 1997-US12116	19970711
W: BR, CA, CN, JP, MX, US				

L86 ANSWER 6 OF 24 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Laundry detergent compositions comprising a specific cellulase and a specific zeolite
SO PCT Int. Appl., 72 pp.
CODEN: PIXXD2
IN Bettiol, Jean-Luc Philippe; Thoen, Christiaan Authur Jacques Kamiel
AN 1999:64890 HCAPLUS
DN 130:126609

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9902635	A1	19990121	WO 1997-US12113	19970711
W: BR, CA, CN, JP, MX, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				

L86 ANSWER 7 OF 24 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

TI Enzymatic laundry detergent and/or fabric care composition.
PI WO 9957250 A1 19991111 (200003)* EN 95 C12N009-00
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW
AU 9872754 A 19991123 (200016) C12N009-00
IN BETTIOL, J P; BOYER, S L; BUSCH, A; SMETS, J

L86 ANSWER 8 OF 24 MEDLINE on STN DUPLICATE 2
TI Comparison of gene structures and enzymatic properties between two endoglucanases from Humicola grisea.
SO Journal of biotechnology, (1999 Jan 22) 67 (2-3) 85-97.
Journal code: 8411927. ISSN: 0168-1656.
AU Takashima S; Iikura H; Nakamura A; Hidaka M; Masaki H; Uozumi T
AN 1999144540 MEDLINE

L86 ANSWER 9 OF 24 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Studies about indigo backstaining during washing with cellulases.
SO Book of Abstracts, 218th ACS National Meeting, New Orleans, Aug. 22-26 (1999), CELL-062 Publisher: American Chemical Society, Washington, D. C.
CODEN: 67ZJA5
AU Andreaus, Juergen; Campos, Rui; Cavaco-Paulo, Artur
AN 1999:539896 HCAPLUS

L86 ANSWER 10 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Modified protein for use in laundry detergents and/or fabric care compositions;
e.g. dextranase, xanthine-oxidase and cecropin-B and e.g. Clostridium cellulovorans or Bacillus agaradherens **cellulose-binding domain** for use in laundry surfactant
AU Bettiol J L; Smets J; Boyer S L
AN 2000-02684 BIOTECHDS
PI WO 9957157 11 Nov 1998

L86 ANSWER 11 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Hybrid protein used in detergents for cleaning fabrics;
hybrid protein containing a Clostridium cellulovorans, **Humicola insolens** or Cellulomonas fimi **cellulose-binding domain** for use in a laundry surfactant
AU Baeck A C; Smets J; Boyer S L
AN 2000-02683 BIOTECHDS
PI WO 9957156 11 Nov 1998

L86 ANSWER 12 OF 24 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Fusion protein comprising α-amylase and a **cellulose-binding domain** for the degradation of starch
SO PCT Int. Appl., 84 pp.
CODEN: PIXXD2
IN Bjornvad, Mads; Pedersen, Sven; Schulein, Martin; Bisgard-Frantzen, Henrik
AN 1998:251260 HCAPLUS
DN 128:318808

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9816633	A1	19980423	WO 1997-DK448	19971013

PI WO 9816633
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR,

GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

EP 950093	A2	19991020	EP 1997-943797	19971013
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FI				
CN 1233286	A	19991027	CN 1997-198640	19971013

L86 ANSWER 13 OF 24 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Cloning and gene sequence of novel endoglucanases from Cellvibrio mixtus and C. gilvus
SO PCT Int. Appl., 118 pp.
CODEN: PIXXD2
IN Bjornvad, Mads Eskelund; Nielsen, Preben
AN 1998:163676 HCAPLUS
DN 128:214198

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9808940	A1	19980305	WO 1997-DK348	19970826
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9739389	A1	19980319	AU 1997-39389	19970826

L86 ANSWER 14 OF 24 MEDLINE on STN DUPLICATE 3
TI Characterization of a cellobiose dehydrogenase from **Humicola insolens.**
SO Biochemical journal, (1998 Feb 15) 330 (Pt 1) 565-71.
Journal code: 2984726R. ISSN: 0264-6021.
AU Schou C; Christensen M H; Schulein M
AN 1998129776 MEDLINE

L86 ANSWER 15 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Producing improved sanitary paper products;
Kraft pulp treatment with **Humicola insolens** or Myceliophthora thermophila cellulase
AU Sharyo M; Sakaguchi H; Onishi M; Takahashi M; Kida K; Tamagawa H; Schuelein M; Franks N E
AN 1997-11013 BIOTECHDS
PI WO 9727363 31 Jul 1997

L86 ANSWER 16 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Forming localized variation of color density in the surface of a dyed cellulosic fabric;
Bacillus sp., Bacillus lautus and **Humicola insolens** cellulase-mediated denim fabric stone-washing without back-staining
AU Onishi M; Fich M; Toft A H; Schuelein M
AN 1997-06280 BIOTECHDS
PI WO 9709410 13 Mar 1997

L86 ANSWER 17 OF 24 HCAPLUS COPYRIGHT 2004 ACS on STN
TI Cellulases with reduced mobility by immobilization or gel incorporation for use in laundry detergents or fabric softeners
SO PCT Int. Appl., 77 pp.
CODEN: PIXXD2
IN Nielsen, Jack Bech; Tikhomirov, Dmitry Feodorovich
AN 1997:145273 HCAPLUS
DN 126:141392

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9701629	A1	19970116	WO 1996-DK284	19960626

W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA

AU 9662988	A1	19970130	AU 1996-62988	19960626
EP 835302	A1	19980415	EP 1996-921912	19960626

R: BE, DE, DK, ES, FR, GB, GR, IT, NL, SE, PT, IE

L86 ANSWER 18 OF 24 MEDLINE on STN DUPLICATE 4
TI Enzymatic properties of cellulases from **Humicola insolens.**
SO Journal of biotechnology, (1997 Sep 16) 57 (1-3) 71-81.
Journal code: 8411927. ISSN: 0168-1656.
AU Schulein M
AN 97475712 MEDLINE

L86 ANSWER 19 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Enzymatic properties of cellulases from **Humicola insolens**;
cellulase e.g. cellobiohydrolase and endo-glucanase characterization and pH activity profile for cellulose hydrolysis
SO J.Biotechnol.; (1997) 57, 1-3, 71-81
CODEN: JBITD4 ISSN: 0168-1656
AU Schuelein M
AN 1997-12446 BIOTECHDS

L86 ANSWER 20 OF 24 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
TI STRUCTURE DETERMINATION AND REFINEMENT OF THE **HUMICOLA-INSOLENS** ENDOGLUCANASE-V AT 1.5 ANGSTROM RESOLUTION
SO ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY, (01 JAN 1996) Vol. 52, Part 1, pp. 7-17.
ISSN: 0907-4449.
AU DAVIES G J (Reprint); DODSON G; MOORE M H; TOLLEY S P; DAUTER Z; WILSON K S; RASMUSSEN G; SCHULEIN M
AN 96:115910 SCISEARCH

L86 ANSWER 21 OF 24 MEDLINE on STN DUPLICATE 5
TI Dynamic light scattering study of the two-domain structure of **Humicola insolens** endoglucanase V.
SO FEBS letters, (1995 Nov 27) 376 (1-2) 49-52.
Journal code: 0155157. ISSN: 0014-5793.
AU Boisset C; Borsali R; Schulein M; Henrissat B
AN 96096785 MEDLINE

L86 ANSWER 22 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Recombinant cellulase variant of a parent cellulase, e.g. **Humicola insolens** 43 kDa cellulase;
prepared by enzyme engineering and useful in surfactant composition in animal feedstuff, paper pulp processing and denim fabric stonewashing
AN 1994-07745 BIOTECHDS
PI WO 9407998 14 Apr 1994

L86 ANSWER 23 OF 24 MEDLINE on STN DUPLICATE 6
TI A novel, small endoglucanase gene, egl5, from Trichoderma reesei isolated by expression in yeast.
SO Molecular microbiology, (1994 Jul) 13 (2) 219-28.
Journal code: 8712028. ISSN: 0950-382X.
AU Saloheimo A; Henrissat B; Hoffren A M; Teleman O; Penttila M
AN 95075308 MEDLINE

L86 ANSWER 24 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN

TI Screening of fungus DNA gene bank, especially of **Humicola insolens**;
cellulase gene cloning and expression for use in surfactant compositi on
AN 1993-11266 BIOTECHDS
PI WO 9311249 10 Jun 1993

=> d ab 18-22

L86 ANSWER 18 OF 24 MEDLINE on STN DUPLICATE 4
AB We present the analysis of the activities towards soluble and insoluble substrates of seven cellulases cloned from the saprophytic fungus **Humicola insolens.** The activity on the soluble polymer substrate carboxymethylcellulose (CMC) was used to determine the pH activity profiles of the five endoglucanases (EG), whereas cellotriose and reduced cellohexaose were used to determine the pH activity profiles of cellobiohydrolase I (CBH) and CBH II. All the EGs show optimal activity between pH 7 and 8.5, while CBH I and CBH II peak around pH 5.5 and 9, respectively. The catalytic activities of five of these cellulases were investigated under neutral and alkaline conditions using reduced cellohexaose as a substrate in a cellobiose oxidase coupled assay. EG I and CBH I both belong to family (7) according to a recent classification of glycosyl hydrolases. They both have activity against cellotriose. Therefore, they were studied using a coupled assay involving glucose oxidase. The activity on insoluble substrate (phosphoric-acid swollen cellulose) was assessed by the formation of reducing groups. The presence of a **cellulose binding domain** (**CBD**) lowers the apparent KM. This can be explained by the dispersing action of **CBD.** However, the **CBD** also reduces the apparent k(cat) probably by slowing down the mobility. EG I, EG II and EG III show similar activity towards CMC and amorphous cellulose, while EG V, EG VI, CBH I and CBH II have the highest catalytic rate on amorphous cellulose. In summary, **Humicola insolens** possesses a battery of cellulose-degrading enzymes which cooperate in the efficient hydrolysis of cellulose.

L86 ANSWER 19 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
AB The enzymatic properties of 7 cellulases (EC-3.2.1.4) cloned from **Humicola insolens** were investigated. Activity on CM-cellulase (CMC) was used to determine pH activity profiles of the 5 endo-glucanases (EGs), whereas cellotriose and reduced cellohexaose were used to determine the pH activity of cellobiohydrolase (CHB, EC-3.2.1.91)-I and -II. All the EGs showed optimal activity between pH 7 and 8.5, while CBH-I and -II peaked around 5.5 and 9, respectively. The catalytic activities of 5 of these cellulase were investigated under neutral and alkaline conditions using reduced cellohexaose as a substrate in a cellobiose-oxidase (EC-1.1.3.25) coupled assay. EG-I and CBH-I show activity against cellotriose. Therefore, they were studied using a coupled assay involving glucose-oxidase (EC-1.1.3.4). The activity on phosphoric-acid swollen cellulose was assessed by reducing group formation. The presence of **cellulose-binding domain** (**CBD**) lowered the apparent kM. **CBD** also reduced the kcat. In summary, H. insolens possesses a battery of cellulose-degrading enzymes which cooperate in cellulose hydrolysis. (35 ref)

L86 ANSWER 20 OF 24 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
AB The structure of the catalytic core of the endoglucanase V (EGV) from **Humicola insolens** has been determined by the method of multiple isomorphous replacement at 1.5 Angstrom resolution. The final model, refined with X-PLOR and PROLSQ, has a crystallographic R factor of 0.163 (R(free) = 0.240) with deviations from stereochemical target values

of 0.012 Angstrom and 0.037 degrees for bonds and angles, respectively. The model was further refined with SHELXL, including anisotropic modelling of the protein-atom temperature factors, to give a final model with an R factor of 0.105 and an R(free) of 0.154. The initial isomorphous replacement electron-density map was poor and uninterpretable but was improved by the use of synchrotron data collected at a wavelength chosen so as to optimize the f '' contribution of the anomalous scattering from the heavy atoms. The structure of H. insolens EGV consists of a six-stranded beta-barrel domain, similar to that found in a family of plant defence proteins, linked by a number of disulfide-bonded loop regions. A long open groove runs across the surface of the enzyme either side of which lie the catalytic aspartate residues. The 9 Angstrom separation of the catalytic carboxylate groups is consistent with the observation that EGV catalyzes the hydrolysis of the cellulose beta(1-->4) links with inversion of configuration at the anomeric C1 atom. This structure is the first representative from the glycosyl hydrolase family 45.

L86 ANSWER 21 OF 24 MEDLINE on STN DUPLICATE 5
AB Endoglucanase V (EG V) of **HUmicola insolens** is composed of a catalytic domain and of a **cellulose-binding domain** linked by a 33 amino acid long peptide rich in Ser, Thr and Pro residues. This work describes the dynamic behavior of the two-domain structure of EG V as revealed by quasi-elastic light scattering experiments. For both the full-length and the isolated catalytic domain, the autocorrelation function is essentially described by a single relaxation mode. The equivalent hydrodynamic radius of the catalytic domain was found to correspond precisely to the dimensions measured from the previously determined three-dimensional structure. The results obtained with the full-length protein allow a description of the two domain structure of EG V similar to that resulting from earlier studies using small angle X-ray scattering on cellulases from Trichoderma reesei. The hydrodynamic dimensions of the entire enzyme can be approximated as an ellipsoid with dimensions of 42 x 133.6 A.

L86 ANSWER 22 OF 24 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
AB A cellulase (EC-3.2.1.4) variant (I) of a parent cellulase in family 45, preferably a Humicola, Trichoderma, Myceliophthora, Penicillium, Irpex, Aspergillus or Fusarium sp. cellulase, especially **Humicola insolens** 43 kDa cellulase, is claimed. Surfactant compositions containing (I) are also claimed. (I) preferably comprises a **cellulose binding domain** (**CBD**), a catalytically active domain (CAD) and a linker for **CBD** and CAD, where at least 1 amino acid residue of the **CBD**, CAD or linker region is deleted or substituted, at least 1 amino acid is added to the linker and/or another **CBD** is added at the opposite end of the CAD. A preferred (I) has at least 1 amino acid in the linker substituted with Thr, Ser or Pro to provide sites for O-glycosylation. (I) has improved alkaline activity, compatibility with surfactant composition ingredients, particulate soil removal, color clarification, defuzzing, depilling, harshness reduction and sensitivity to anionic surfactants and peroxidase (EC-111.1.7) bleaching systems and is useful for surfactant compositions in textile treatment, paper pulp processing, animal feeds and for stonewashing denim fabric. (83pp)

=> s (binding or affinity) and l61 and l24
FILE 'MEDLINE'
681369 BINDING
185677 AFFINITY
L87 2 (BINDING OR AFFINITY) AND L50 AND L13

FILE 'SCISEARCH'
631772 BINDING

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        154199 AFFINITY
L88          6 (BINDING OR AFFINITY) AND L51 AND L14

FILE 'LIFESCI'
        218703 BINDING
         65830 AFFINITY
L89          1 (BINDING OR AFFINITY) AND L52 AND L15

FILE 'BIOTECHDS'
         32425 BINDING
         13666 AFFINITY
L90          1 (BINDING OR AFFINITY) AND L53 AND L16

FILE 'BIOSIS'
        609977 BINDING
        199201 AFFINITY
L91          2 (BINDING OR AFFINITY) AND L54 AND L17

FILE 'EMBASE'
        596117 BINDING
        188439 AFFINITY
L92          2 (BINDING OR AFFINITY) AND L55 AND L18

FILE 'HCAPLUS'
        832290 BINDING
        265012 AFFINITY
L93          2 (BINDING OR AFFINITY) AND L56 AND L19

FILE 'NTIS'
          9626 BINDING
          2446 AFFINITY
L94          0 (BINDING OR AFFINITY) AND L57 AND L20

FILE 'ESBIOBASE'
        224246 BINDING
         67238 AFFINITY
L95          2 (BINDING OR AFFINITY) AND L58 AND L21

FILE 'BIOTECHNO'
        277750 BINDING
         87816 AFFINITY
L96          1 (BINDING OR AFFINITY) AND L59 AND L22

FILE 'WPIDS'
         98243 BINDING
         27438 AFFINITY
L97          1 (BINDING OR AFFINITY) AND L60 AND L23

TOTAL FOR ALL FILES
L98         20 (BINDING OR AFFINITY) AND L61 AND L24

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PROCESSING COMPLETED FOR L98
L99           7 DUP REM L98 (13 DUPLICATES REMOVED)

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L99  ANSWER 1 OF 7  SCISEARCH  COPYRIGHT (c) 2004 The Thomson Corporation.  on
     STN
TI   Dimension, shape, and conformational flexibility of a two domain fungal
     cellulase in solution probed by small angle X-ray scattering
SO   JOURNAL OF BIOLOGICAL CHEMISTRY, (25 OCT 2002) Vol. 277, No. 43, pp.
     40887-40892.
     Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC, 9650 ROCKVILLE
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ISSN: 0021-9258.
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AN 2002:890802 SCISEARCH

L99 ANSWER 2 OF 7 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
TI Chemical entities for fabric care comprises chemical components linked to a cellulose **binding** domain which has specified **binding** constants;
also claimed are a laundry surfactant and/or fabric care composition
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AN 2000-09604 BIOTECHDS
PI WO 2000018898 6 Apr 2000

L99 ANSWER 3 OF 7 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
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L99 ANSWER 4 OF 7 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
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L99 ANSWER 5 OF 7 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN
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L99 ANSWER 6 OF 7 MEDLINE on STN DUPLICATE 2
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L99 ANSWER 7 OF 7 MEDLINE on STN DUPLICATE 3
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=> d ab 14,16,21,25,31,36,54,57,61,64,68,70,85,79,82,94,97 149

L49 ANSWER 14 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AB **Cellulose-binding domains** (**CBDs**) are structurally and functionally independent, noncatalytic modules found in many cellulose or hemicellulose degrading enzymes. Recent biotechnological applications of the **CBDs** include facilitated protein immobilization on cellulose supports. In some occasions there have been concerns about the stability of the **CBD** driven immobilization. Here we have studied the chromatographic behavior of variants of the Trichoderma reesei cellobiohydrolase **CBD** belonging to family 1. Both **CBDs** fused to antibody fragments and isolated **CBDs** were studied and compared. Tritium labeling by reductive methylation was used as a sensitive detection method. The fusion protein as well as the isolated **CBD** was found to leak from the column at a rate of 0.3-0.5% of the immobilized protein per column volume. However, the leakage could be overcome by using two **CBDs** instead of a single **CBD** for the immobilization. In this way leakage was reduced to less than 0.01% per column volume. The improved immobilization could also be seen as a decreased migration of the protein down the column in extended washes. (C) 1998 John Wiley & Sons, Inc.

L49 ANSWER 16 OF 103 MEDLINE on STN DUPLICATE 6

AB **Cellulose-binding domains** (**CBDs**) are discrete protein modules found in a large number of carbohydrolases and a few nonhydrolytic proteins. To date, almost 200 sequences can be classified in 13 different families with distinctly different properties. **CBDs** vary in size from 4 to 20 kDa and occur at different positions within the polypeptides; N-terminal, C-terminal and internal. They have a moderately high and specific **affinity** for insoluble or soluble cellulosics with dissociation constants in the low micromolar range. Some **CBDs** bind irreversibly to cellulose and can be used for applications involving immobilization, others bind reversibly and are more useful for separations and purifications. Dependent on the **CBD** used, desorption from the matrix can be promoted under various different conditions including denaturants (urea, high pH), water, or specific competitive ligands (e.g. cellobiose). Family I and IV **CBDs** bind reversibly to cellulose in contrast to family II and III **CBDs** which are in general, irreversibly bound. The **binding** of family II **CBDs** (**CBD**(Cex)) to **crystalline cellulose** is characterized by a large favourable increase in entropy indicating that dehydration of the sorbent and the protein are the major driving forces for **binding.** In contrast, **binding** of family IV **CBDs** (**CBD**(N1)) to amorphous or soluble cellulosics is driven by a favourable change in enthalpy which is partially offset by an unfavourable entropy change. Hydrogen bond formation and van der Waals interactions are the main driving forces for **binding.** **CBDs** with **affinity** for **crystalline cellulose** are useful tags for classical column **affinity** chromatography. The **affinity** of **CBD**(N1) for soluble cellulosics makes it suitable for use in large-scale aqueous two-phase **affinity** partitioning systems.

L49 ANSWER 21 OF 103 BIOSIS COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 10

L49 ANSWER 25 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AB The surface diffusion rate of bacterial cellulases from Cellulomonas

fimi on cellulose was quantified using fluorescence recovery after photobleaching analysis. Studies were performed on an exo-beta-1-4-glycanase (Cex), an endo-beta-1-4-glucanase (CenA), and their respective isolated **cellulose-binding domains** (**CBDs**). Although these **cellulose-binding domains** hind irreversibly to microcrystalline cellulose, greater than 70% of bound molecules are mobile on the cellulose surface. Surface diffusion rates are dependent on surface coverage and range from a low of 2 x 10(-11) to a maximum of 1.2 x 10(-10) cm(2)/s. The fraction of mobile molecules increases only slightly with increasing fractional surface coverage density. Results demonstrate that the packing of C. fimi cellulases and their isolated **binding** domains onto the cellulose surface is a dynamic process. This suggests that the exclusion of potential **CBD binding** sites on the cellulose due to steric effects of neighboring bound **CBDs** may not fully explain the apparent negative cooperativity exhibited in **CBD** adsorption isotherms. Comparison with the kinetics of cellulase hydrolysis of crystalline substrate suggests that surface diffusion rates do not limit cellulase activity.

L49 ANSWER 31 OF 103 MEDLINE on STN DUPLICATE 16

AB Three-dimensional solution structures for three engineered, synthetic **CBDs** (Y5A, Y31A, and Y32A) of cellobiohydrolase I (CBHI) from Trichoderma reesei were studied with nuclear magnetic resonance (NMR) and circular dichroism (CD) spectroscopy. According to CD measurements the antiparallel beta-sheet structure of the **CBD** fold was preserved in all engineered peptides. The three-dimensional NMR-based structures of Y31A and Y32A revealed only small local changes due to mutations in the flat face of **CBD**, which is expected to bind to **crystalline cellulose.** Therefore, the structural roles of Y31 and Y32 are minor, but their functional importance is obvious because these mutants do not bind strongly to cellulose. In the case of Y5A, the disruption of the structural framework at the N-terminus and the complete loss of **binding affinity** implies that Y5 has both structural and functional significance. The number of aromatic residues and their precise spatial arrangement in the flat face of the type I **CBD** fold appears to be critical for specific **binding.** A model for the **CBD binding** in which the three aligned aromatic rings stack onto every other glucose ring of the cellulose polymer is discussed.

L49 ANSWER 36 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 19

AB Most cellulolytic enzymes consist of distinct catalytic and **cellulose-binding domains** (**CBDs**). Similar domain structures are also found in enzymes degrading other insoluble carbohydrates such as raw starch and chitin. Such **binding** domains improve the **binding** and facilitate the activity of the catalytic domain on the insoluble but not on soluble substrates, Based on their amino acid sequence similarities, the **CBDs** have been divided into several different families. Structure determination and subsequent mutagenesis studies have revealed that **CBDs** rely on several aromatic amino acids for **binding** to the cellulose surfaces. The **CBDs binding** to **crystalline cellulose** have different topologies but share similar rigid backbone structures for correct positioning of the side chains required for the substrate recognition and **binding.** **CBDs** represent ideal **affinity** tags for specific immobilisation of various other proteins to cellulose. Furthermore, improved understanding and control of their action will be important for the improvement of the biotechnological value of cellulolytic enzymes. (C) 1997 Elsevier Science B.V.

L49 ANSWER 54 OF 103 HCAPLUS COPYRIGHT 2004 ACS on STN

AB A review with 18 refs. on the biodegrdn. of **crystalline cellulose** (I) with enzymes is presented. The filamentous fungus Trichoderma reesei produces a potent set of cellulolytic enzymes. The key enzymes in crystal erosion are 2 cellobiohydrolases (CBH), which bind tightly to the I surface and liberate cellobiose from the opposite chain ends. Both enzymes contain a large catalytic domain and a distinct I-**binding** domain (**CBD**). The catalytic mechanisms of CBHII by site-directed mutagenesis of several catalytic and substrate-**binding** residues in its active site are discussed. **CBD** -I interactions are examined by use of synthetic peptides, site-directed mutants, and fusion proteins. This shows how insol. crystalline I is attacked by enzymes, and facilitates development of novel applications for I-based materials.

L49 ANSWER 57 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN

AB A family II **cellulose-binding domain** (**CBD**) of an exoglucanase/xylanase (Cex) from the bacterium Cellulomonas fimi was replaced with the family I **CBD** of cellobiohydrolase I (CbhI) from the fungus Trichoderma reesei. Expression of the hybrid gene in Escherichia coli yielded up to 50 mg of the hybrid protein, CexCBD(CbhI), per liter of culture supernatant. The hybrid was purified to homogeneity by **affinity** chromatography on cellulose, The relative association constants (K-r) for the **binding** of Cex, CexCBD(CbhI), the catalytic domain of Cex (p33), and CbhI to bacterial microcrystalline cellulose (BMCC) were 14.9, 7.8, 0.8, and 10.6 liters g(-1) respectively. Cex and CexCBD(CbhI) had similar substrate specificities and similar activities on crystalline and amorphous cellulose. Both released predominantly cellobiose and cellotriose from amorphous cellulose. CexCBD(CbhI) was two to three times less active than Cex on BMCC, but significantly more active than Cex on soluble cellulose acid on xylan. Unlike Cex, the hybrid protein neither bound to alpha-chitin nor released small particles from dewaxed cotton fibers.

L49 ANSWER 61 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN

AB Recombinant protein purification may be achieved using a **cellulose-binding domain** (**CBD**) that binds to **crystalline cellulose** which allows the purification and immobilization of **CBD** fusion proteins. Plasmid pLCM was constructed encoding a **CBD**-Clostridium cellulovorans cellulase (EC-3.2.1.4) fusion protein. After **binding** of the **CBD**-cellulase fusion protein to cellulose (Avicel) and washing with buffer, the presence of the purified fusion protein on cellulose was confirmed by elution from cellulose with SDS sample loading buffer and by SDS-PAGE. The purified fusion protein was bound to cellulose, which was used for the enzyme immobilization system. The **CBD**-cellulase fusion protein was active when the fusion protein was bound to cellulose. Factor-Xa was used for **CBD**-cellulase fusion protein cleavage at the specific linkage site (Ile-Glu-Gly-Arg-*-X). SDS-PAGE and Western blotting experiments confirmed the elution of cellulase from the cellulose-bound fusion protein. The eluted cellulase was active on CM-cellulose plates. This system allows **binding** of an active fusion protein to cellulose and purification of the target protein (cellulase). (0 ref)

L49 ANSWER 64 OF 103 BIOTECHDS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN

AB The 4 cellulases (endoglucanases, EC-3.2.1.4), 2 cellobiohydrolases (EC-3.2.1.91), endo-1,4-beta-D-xylanase (EC-3.2.1.8) and a mixed function exoglucanase-xylanase of Cellulomonas fimi are modular proteins comprising 2-6 domains. All contain a catalytic domain (CD) and a **cellulose-binding domain** (**CBD**) that function independently when separated by proteolysis or genetic engineering. The CDs have weak **affinity** for substrate, relative to the **CBDs**, and catalyze hydrolysis of glycosidic

bonds with inversion or retention of anomeric configuration. The family II **CBDs** adsorb to both crystalline and amorphous cellulose (except for xylanase-D **CBD** which adsorbs only to **crystalline cellulose**). The family IV **CBD** from endoglucanase CenC adsorbs only to amorphous cellulose. Adsorption is strongly dependent on aromatic amino acids, especially tryptophans, which are conserved in nearly all family II **CBDs.** The endoglucanase CenA **CBD** has a disruptive effect on cotton fibers. The **binding** of family II **CBDs** to cellulose is stable enough for them to be used as **affinity** tags for protein purification and enzyme immobilization. (54 ref)

L49 ANSWER 68 OF 103 MEDLINE on STN DUPLICATE 34

AB Cellulose-**binding** protein A (CbpA) has been previously shown to mediate the interaction between **crystalline cellulose** substrates and the cellulase enzyme complex of Clostridium cellulovorans. CbpA contains a family III **cellulose-binding domain** (**CBD**) which, when expressed independently, binds specifically to **crystalline cellulose.** A series of N- and C-terminal deletions and a series of small internal deletions of the **CBD** were created to determine whether the entire region previously described as a **CBD** is required for the cellulose-**binding** function. The N- and C-terminal deletions reduced **binding affinity** by 10- to 100-fold. Small internal deletions of the **CBD** resulted in substantial reduction of **CBD** function. Some, but not all, point mutations throughout the sequence had significant disruptive effects on the **binding** ability of the **CBD.** Thus, mutations in any region of the **CBD** had effects on the **binding** of the fragment to cellulose. The results indicate that the entire 163-amino-acid region of the **CBD** is required for maximal **binding** to **crystalline cellulose.**

L49 ANSWER 70 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 36

AB Cellulases expressed by Cellulomonas fimi consist of a catalytic domain and a discrete non-catalytic **cellulose-binding domain** (**CBD**). To establish whether **CBDs** are common features of plant cell-wall hydrolases from C. fimi, the molecular architecture of xylanase D (XYLD) from this bacterium was investigated. The gene encoding XYLD, designated xynD, consisted of an open reading frame of 1936 bp encoding a protein of M, 68000. The deduced primary sequence of XYLD was confirmed by the size (64 kDa) and N-terminal sequence of the purified recombinant xylanase. Biochemical analysis of the purified enzyme revealed that XYLD is an endoacting xylanase which displays no detectable activity against polysaccharides other than xylan. The predicted primary structure of XYLD comprised an hi-terminal signal peptide followed by a 190-residue domain that exhibited significant homology to Family-G xylanases. Truncated derivatives of xynD encoding the N-terminal 193 amino acids of mature XYLD directed the synthesis of a functional xylanase, confirming that the 190-residue N-terminal sequence constitutes the catalytic domain. The remainder of the enzyme consisted of two approximately 90-residue domains, which exhibited extensive homology with each other, and limited sequence identity with **CBDs** from other polysaccharide hydrolases. Between the two putative **CBDs** is a 197-amino-acid sequence that exhibits substantial homology with Rhizobium NodB proteins. The four discrete domains in XYLD were separated by either threonine/prolineor novel glycine-rich linker regions. Although full-length XYLD adsorbed to cellulose, truncated derivatives of the enzyme lacking the C-terminal **CBD** hydrolysed xylan but did not bind to cellulose. Fusion of the C-terminal domain to glutathione-S-transferase generated hybrid proteins that bound to **crystalline cellulose**, but not to amorphous cellulose or xylan. The location of **CBDs** in a C. fimi xylanase indicates that domains of this type are not restricted to cellulases, but are widely distributed between

hemicellulases also, and therefore play a pivotal role in the activity of the whole repertoire of plant cell-wall hydrolases. The role of the NodB homologue in XYLD is less certain.

L49 ANSWER 85 OF 103 MEDLINE on STN DUPLICATE 49
AB Endoglucanase C (CenC) from Cellulomonas fimi binds to cellulose and to Sephadex. The enzyme has two contiguous 150-amino-acid repeats (N1 and N2) at its N-terminus and two unrelated contiguous 100-amino-acid repeats (C1 and C2) at its C-terminus. Polypeptides corresponding to N1, N1N2, C1, and C1C2 were produced by expression of appropriate cenC gene fragments in Escherichia coli. N1N2, but not N1 alone, binds to Sephadex; both polypeptides bind to Avicel, (a heterogeneous cellulose preparation containing both crystalline and non-crystalline components). Neither C1 nor C1C2 binds to Avicel or Sephadex. N1N2 and N1 bind to regenerated ('amorphous') cellulose but not to bacterial **crystalline cellulose**; the **cellulose-binding domain** of C. fimi exoglucanase Cex binds to both of these forms of cellulose. Amino acid sequence comparison reveals that N1 and N2 are distantly related to the **cellulose-binding domains** of Cex and C. fimi endoglucanases A and B.

L49 ANSWER 79 OF 103 SCISEARCH COPYRIGHT (c) 2004 The Thomson Corporation. on STN DUPLICATE 45
AB The **cellulose-binding domain** (**CBD** (CenC)) of endoglucanase C (CenC) from Cellulomonas fimi binds to amorphous (phosphoric acid-swollen) cellulose (PASC) but not to bacterial microcrystalline cellulose (BMCC), whereas that of endoglucanase A (**CBD**(CenA)) binds to both forms of cellulose. Substitution of **CBD**(CenC) for **CBD**(CenA) in endoglucanase A (CenA) affects the activity of the enzyme on different forms of cellulose. The hybrid enzyme (CenC''A) is less active than CenA on BMCC and Avicel. The two forms of the enzyme have similar activity on PASC. CenC''A is more active than CenA on cellulose azure and carboxymethyl cellulose. CenC''A binds to phosphoric acid-swollen cellulose but not to **crystalline cellulose.** The hybrid enzyme is less sensitive than CenA to C. fimi protease, probably as a consequence of replacement of the prolyl-threonyl linker of CenA by a triprolyl linker from CenC.

L49 ANSWER 82 OF 103 MEDLINE on STN DUPLICATE 46
AB CenA is a bacterial cellulase (beta-1,4-glucanase) comprised of a globular catalytic domain joined to an extended **cellulose-binding domain** (**CBD**) by a short linker peptide. The adsorption of CenA and its two isolated domains to **crystalline cellulose** was analyzed. CenA and **CBD.**PTCenA' (the **CBD** plus linker) adsorbed rapidly to cellulose at 30 degrees C, and no net desorption of protein was observed during the following 16.7 h. There was no detectable adsorption of the catalytic domain. Scatchard plots of adsorption data for CenA and for **CBD.**PTCenA were nonlinear (concave upward). The adsorption of CenA and **CBD** .PTCenA exceeded 7 and 8 mumol/g cellulose, respectively, but saturation was not attained at the highest total protein concentrations employed. A new model for adsorption was developed to describe the interaction of a large ligand (protein) with a lattice of overlapping potential **binding** sites (cellobiose residues). A relative equilibrium association constant (Kr) of 40.5 and 45.3 liter.g cellulose-1 was estimated for CenA and **CBD.**PTCenA, respectively, according to this model. A similar Kr value (33.3 liter.g-1) was also obtained for Cex, a Cellulomonas fimi enzyme which contains a related **CBD** but which hydrolyzes both beta 1,4-xylosidic and beta-1,4-glucosidic bonds. It was estimated that the **CBD** occupies approximately 39 cellobiose residues on the cellulose surface.

L49 ANSWER 94 OF 103 MEDLINE on STN DUPLICATE 53
AB Mature endoglucanase E (EGE) from Clostridium thermocellum consists of 780

amino acid residues and has an Mr of 84,016. The N-terminal 334 amino acids comprise a functional catalytic domain. Full-length EGE bound to **crystalline cellulose** (Avicel) but not to xylan. Bound enzyme could be eluted with distilled water. The capacity of truncated derivatives of the enzyme to bind cellulose was investigated. EGE lacking 109 C-terminal residues (EGEd) or a derivative in which residues 367-432 of the mature form of the enzyme had been deleted (EGEb), bound to Avicel, whereas EGEa and EGEc, which lack 416 and 246 C-terminal residues respectively, did not. The specific activity of EGEa, consisting of the N-terminal 364 amino acids, was 4-fold higher than that of the full-length enzyme. The truncated derivative also exhibited lower **affinity** for the substrate beta-glucan than the full-length enzyme. It is concluded that EGE contains a **cellulose-binding domain**, located between residues 432 and 671, that is distinct from the active site. The role of this substrate-**binding** domain is discussed.

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AB Fusarium, Humicola and Myceliopthera cellulases (EC-3.2.1.4) have an alkaline pH optimum, and the enzyme complexes are as complicated as that of Trichoderma spp. Conventional purification procedures combined with immunoaffinity purification and reversed-phase HPLC gave monocomponent cellulases and hemicellulases. The cellulases were partly of the cellobiohydrolase (EC-3.2.1.91) type (degrading highly **crystalline cellulose** and forming cellobiose) when the enzyme consisted of both the catalytic core and the **cellulose binding domain** (**CBD**). The other main group of cellulases consisted of endoglucanases, which do not degrade highly **crystalline cellulose** even in the presence of **CBD**, but degrade only amorphous cellulose. Both types of enzyme, with and without **CBD**, degraded soluble cellodextrins. Substituted cellulose, such as CM-cellulose, was only degraded by endoglucanases. The cooperation of the highly purified cellulases was described. (0 ref)

=> log y

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